Forensic Science International: Genetics Supplement Series 5 (2015) e650–e652

Contents lists available at ScienceDirect

Forensic Science International: Genetics Supplement Series

journal homepage: www.elsevier.com/locate/FSIGSS

# A comparison between Yfiler® and RM Y-STRs in United Arab Emirates population

R. Alghafri[a,*], S. Alhammadi[b], K. Amiri[b]

[a] General Department of Forensic Sciences and Criminology, Dubai Police General Head Quarters, Dubai, United Arab Emirates
[b] Biology Department, College of Science, UAE University, Al Ain, United Arab Emirates

ARTICLE INFO

*Article history:*
Received 27 August 2015
Received in revised form 15 September 2015
Accepted 7 October 2015
Available online 20 October 2015

*Keywords:*
Yfiler
Y Chromosome
Rapidly
Mutating
Y-STR
Population
Dubai
UAE

ABSTRACT

Rapidly Mutating Y-STRs (RM Y-STR) were proven to have significantly higher resolution in worldwide populations when compared to commonly used Y-STR kits. In order to contribute to the research that has been conducted so far, RM Y-STRs were investigated in parallel with Yfiler® kit in 327 male individuals from United Arab Emirates population. Such population is considerably isolated where Yfiler® and Powerplex® Y haplotypes were found to be shared between distantly related as well as non-related male individuals. In the present study, a comparison between Y-STR markers included in Yfiler® kit (DYS456, DYS389I, DYS390, DYS389II, DYS458, DYS19, DYS385, DYS393, DYS391, DYS439, DYS635, DYS392, YGATAH4, DYS437, DYS438, DYS448) with RM Y-STRs (DYF387S1, DYF399S1, DYF403S1a/b, DYF404S1, DYS449, DYS518, DYS526a/b, DYS547, DYS570, DYS576, DYS612, DYS626, and DYS627) is conducted. RM Y-STRs were analysed using previously published methods. Forensic parameters were calculated for each set of markers, including discrimination capacity, haplotype diversity and gene diversity, using Arlequin v3.5 software.



## 1. Introduction

Y chromosome STR profiling is a very common method which is used in forensic investigations, especially in sexual assault cases where male fraction of samples are hardly recovered. Yfiler® is one of the widely used multiplex assays in forensic laboratories. Recently a set of 13 markers were discovered which demonstrate significantly higher mutation rate than conventional markers, a feature which has been proven to be effective in discriminating non-relatives males populations as well as close male relatives [1]. Although some of these markers were incorporated in the newly released commercially available multiplex assays, it is still important to investigate the efficiency of these markers in different populations before adopting them for routine analysis. This study presents a parallel comparison between Yfiler® assay and RM Y-STR.

## 2. Materials and methods

### 2.1. Samples collection and extraction

Buccal swabs were collected from 327 individuals of national Arab's in the UAE population as part of Y chromosome polymorphism in UAE population study [2]. Briefly, DNA was extracted from samples using the Biorobot Universal System from Qiagen® with silica membrane matrix method. Quantification step was performed using Quantifiler™ DNA Quantification Kit using a 7500 Real Time System (Applied Biosystems) following the manufacturer protocol.

### 2.2. Amplification and detection

Three multiplexes were used to analyse each sample following previously published methods in order to obtain the 13 markers of RM Y-STRs [1]. Each multiplex was performed in a volume of 10 μl. Previously genotyped male positive controls along with negative controls were used during amplification to ensure quality of the analysis. PCR products were analyzed by capillary electrophoresis by an ABI 3500 Genetic Analyzer for fragment length determination of the products using POP-4™ polymer and LIZ500™ as internal size standard.

* Corresponding author.
*E-mail address:* r.alghafri@hotmail.co.uk (R. Alghafri).

http://dx.doi.org/10.1016/j.fsigss.2015.10.012
1875-1768/

**Table 1**
Forensic parameters for Yfiler® and RM Y-STRs in UAE Arab's populations.

| Forensic parameters | Yfiler® | RM Y-STRs |
|---|---|---|
| Number of samples | 327 | 327 |
| Number of haplotypes | 283 | 327 |
| Number of unique haplotypes | 253 | 327 |
| Discrimination capacity (%) | 89.40% | 100% |
| Haplotypes diversity | 0.98 | 1 |

**Table 2**
Gene diversity for Yfiler® and RM Y-STRs in UAE Arab's populations.

| Yfiler® Loci | Gene diversity | RM Y-STRs Loci | Gene diversity |
|---|---|---|---|
| DYS456 | 0.8405 | DYF387S1 | 0.9212 |
| DYS389I | 0.5898 | DYF399S1 | 0.9926 |
| DYS390 | 0.8360 | DYF403S1a | 0.9812 |
| DYS389II | 0.8249 | DYF403S1b | 0.8979 |
| DYS458 | 0.9262 | DYF404S1 | 0.8257 |
| DYS19 | 0.7451 | DYS449 | 0.8718 |
| DYS385a/b | 0.9512 | DYS518 | 0.8382 |
| DYS393 | 0.7216 | DYS526a | 0.8267 |
| DYS391 | 0.5906 | DYS526b | 0.8821 |
| DYS439 | 0.7856 | DYS547 | 0.7812 |
| DYS635 | 0.8357 | DYS570 | 0.7325 |
| DYS392 | 0.4369 | DYS576 | 0.7333 |
| YGATAH4 | 0.7637 | DYS612 | 0.8199 |
| DYS437 | 0.4777 | DYS626 | 0.6211 |
| DYS438 | 0.7314 | DYS627 | 0.8021 |
| DYS448 | 0.6910 | | |

### 2.3. Statistics analysis

Forensic parameters including discrimination capacity (DC), haplotype diversity (HD) and gene diversity (GD) were calculated using Arlequin v3.5 software [3].

## 3. Results and discussion

Among the 327 Arab's male individuals from the UAE population investigated, 327 distinguishable haplotypes were observed with RM Y-STR (Discrimination capacity of 100%) compared to 253 distinguishable haplotypes observed with Yfiler® (Discrimination capacity of 89.4%) shown in Table 1. This result represents a significant difference of 10% increase in resolution, between the two sets of markers (paired $t$-test, $t = -3.994$, $p = 0.001$). This result is in agreement with previous studies conducted using RM Y-STR on worldwide populations [1,4]. Extremely high resolution is explained by the high rate of mutation which is likely introducing new haplotypes in almost every generation and therefore increasing gene diversity (Table 2) (Fig. 1). Comparing haplotypes produced in this study with a previously published database of 12272 RM Y-STR haplotypes [4], there was no shared haplotypes between UAE Arab's populations and other populations, which also reflect the uniqueness of haplotypes across populations. These findings suggest that the set of 13 RM Y-STRs has great value in forensic investigations. Therefore, application of new generation multiplex assay which has incorporated some or all of these markers is highly recommended in forensic laboratories.

## Conflict of interest

None.

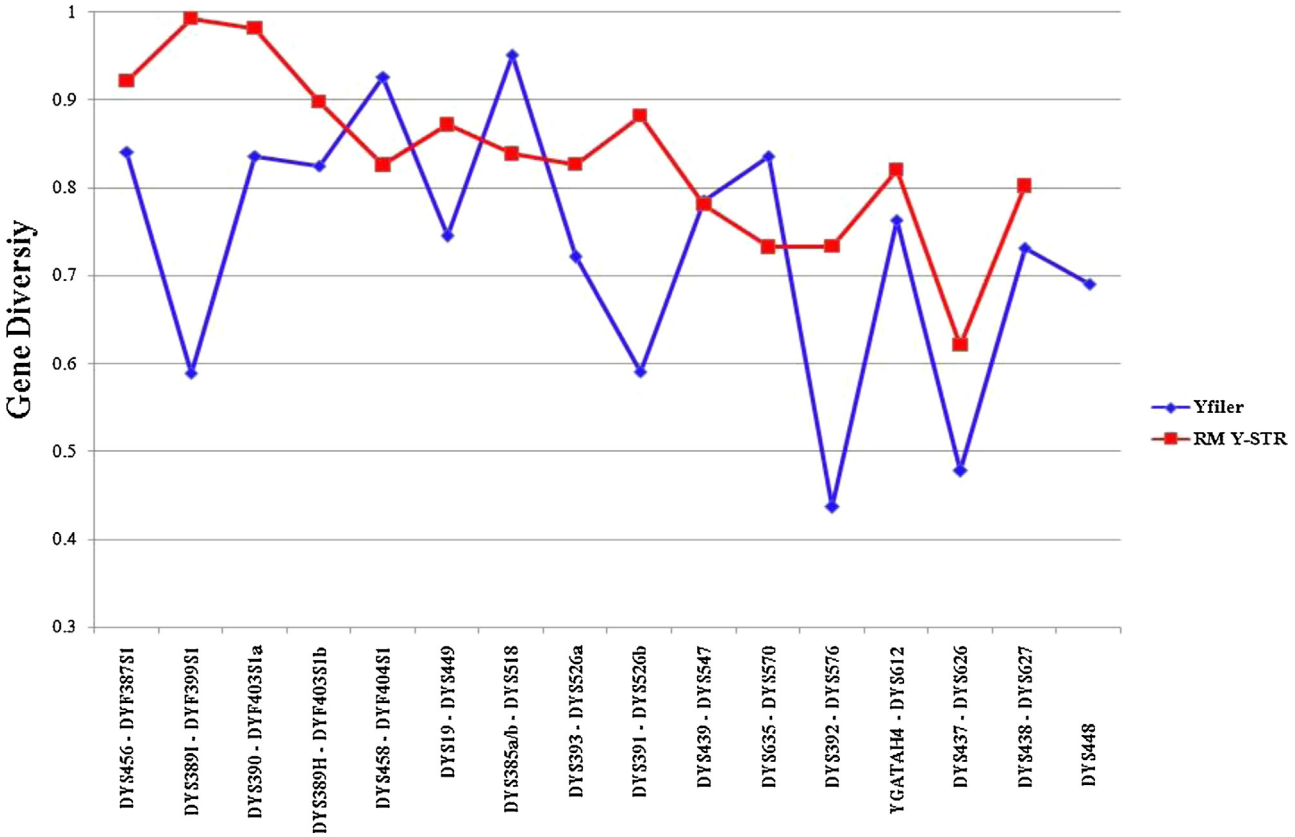


**Fig. 1.** Gene diversity for Yfiler® and RM Y-STRs in UAE Arab's population.

## Acknowledgment

We would like to humbly thank Dubai Government for enabling grant support for this project. We also would like to acknowledge Abu Dhabi Police General Head Quarters and United Arab Emirates University (Internal Research Grant COS/IRG-2012) for financial and technical support.

## References

[1] Kaye N. Ballantyne, Victoria Keerl, Andreas Wollstein, Ying Choi, Sofia B. Zuniga, Arwin Ralf, Mark Vermeulen, Peter de Knijff, Manfred Kayser, A new future of forensic Y-chromosome analysis: Rapidly mutating Y-STRs for differentiating male relatives and paternal lineages, Forensic Sci. Int. Genet. 6 (2) (March 2012) 208–218.

[2] Safa Y. Alhammadi, Ahmed A. Almarzoqi, AbdulMajeed S. Khajah, Ibrahim A. Alhosani, Huda Shaheen, Khaled M. Amiri, Y-chromosome polymorphisms in the United Arab Emirates Population, (Master Dissertation) 2014.

[3] L. Excoffier, H.E.L. Lischer, Arlequin suite ver 3.5: a new series of programs to performpopulation genetics analyses under Linux and Windows, Mol. Ecol. Resour. 10 (2010) 564–567.

[4] K.N. Ballantyne, et al., Toward male individualization with rapidly mutating Y-chromosomal short tandem repeats, Hum. Mutat. 35 (2014) 1021–1032.